

In the Claims:

Cancel Claims 12-14 and add new Claims 17 and 18.

17. (new) An assay method for detecting a predetermined nucleic acid sequence in a sample, comprising:

- Sub B1
- a)
- a'
- providing a sample containing nucleic acids, and a single stranded oligonucleotide probe having a sequence complementary to the predetermined nucleic acid sequence to be detected, the single stranded oligonucleotide probe comprising at least 10 bases, wherein the first base of the single stranded oligonucleotide probe is conjugated to a first fluorescent moiety and the second base of the single stranded oligonucleotide probe is conjugated to a second fluorescent moiety, the first and second bases being positioned so that upon excitation of the first fluorescent moiety, the excitation energy is transferred to the second fluorescent moiety, whereupon the second fluorescent moiety fluoresces with peak fluorescence at a wavelength which differs from the fluorescent peak of the first fluorescent moiety;
  - b) contacting the sample containing nucleic acids with the single stranded oligonucleotide probe, under conditions where complementary single stranded nucleic acids hybridize, and unhybridized single stranded oligonucleotides are hydrolytically digested; and
  - c) measuring fluorescent transfer between the first fluorescent moiety and the second fluorescent moiety of the oligo of step a), subsequent to step b).

18. (new) The assay method of Claim 17 wherein the first base and the second base of the single stranded oligonucleotide probe of step a) are separated by about 15 bases.